

Applied deep learning for interferometric microscopy: complex U-net.

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Key words : Label-free microscopy, deep learning, quantitative phase, interferometry, mitochondria.

Label-free imagery grants non-specific imaging of the entirety of cell components. It however struggles to obtain specific imagery of particular molecular species. Without resorting to slow non-linear methods and/or requiring a strong excitation fluence [1], the main challenges for label-free microscopy are now (i) to improve the ability to discriminate two cellular components and (ii) to unravel the enormous amount of information within an image in order to make it specific.

Over the last years, the use of convolutive neural networks has been largely adopted for most of the imagery segmentation topics. In particular, the so-called U-Net architecture [2], which adds an expansive decoder to the more classical contracting convolutive network, gave access to localized information as well as its context. The use of this architecture allows for specific label prediction through networks trained with relatively small datasets, for all kind of microscopy acquisition, as long as we can provide an objective to reach either by manual annotations or by fluorescence imaging, the latest being the case we study.

Quantitative phase microscopy using interferometry [3] uses the signal amplitude and phase data together to retrieve very-high sensitivity quantitative information. We adapted the existing deep learning algorithms to allow for complex input data.

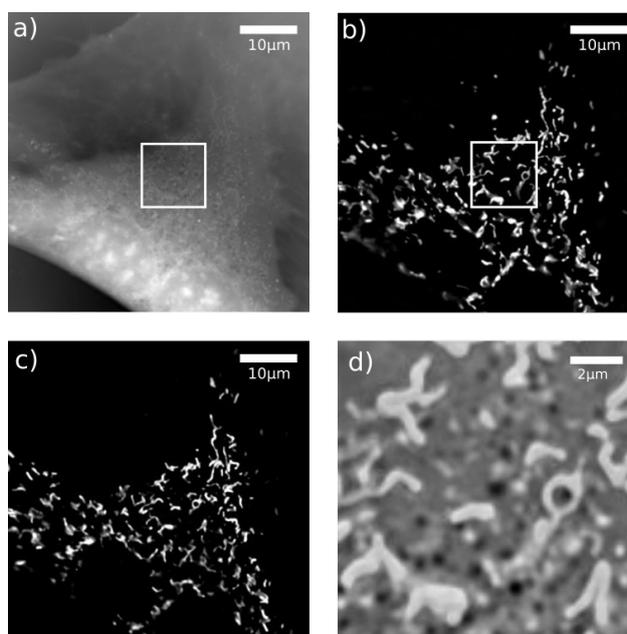


Fig.1: Images of a fibroblast cell a) in quantitative phase phase, b) fluorescence of mitochondria, c) algorithm prediction of mitochondria localization. d) Zoom over a zone displaying several types of organelles: merge of quantitative phase and fluorescence image.

Here we present the impact of the use of the whole electromagnetic field coupled with appropriate learning metrics in a U-Net architecture for label-free mitochondrial identification and dynamics study.

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